05-90
1019

#3

RAW SEQUENCE LISTING   DATE: 10/16/2001
PATENT APPLICATION: US/09/934,586   TIME: 13:54:13

Input Set : **N:\Crf3\RULE60\09934586.txt**
Output Set: **N:\CRF3\10162001\I934586.raw**

SEQUENCE LISTING

```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Au-Young, Janice
 7      (ii) TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
 9     (iii) NUMBER OF SEQUENCES: 26
11      (iv) CORRESPONDENCE ADDRESS:
12           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
13           (B) STREET: 3174 Porter Drive
14           (C) CITY: Palo Alto
15           (D) STATE: CA
16           (E) COUNTRY: U.S.
17           (F) ZIP: 94304
19       (v) COMPUTER READABLE FORM:
20           (A) MEDIUM TYPE: Diskette
21           (B) COMPUTER: IBM Compatible
22           (C) OPERATING SYSTEM: DOS
23           (D) SOFTWARE: FastSEQ Version 1.5
25      (vi) CURRENT APPLICATION DATA:
26           (A) APPLICATION NUMBER: US/09/934,586      C-->
27           (B) FILING DATE: 23-Aug-2001               C-->
28     (vii) PRIOR APPLICATION DATA:
29           (A) APPLICATION NUMBER: 09/225,080
30           (B) FILING DATE: 1999-01-04
32    (viii) ATTORNEY/AGENT INFORMATION:
33           (A) NAME: Billings, Lucy J.
34           (B) REGISTRATION NUMBER: 36,749
35           (C) REFERENCE/DOCKET NUMBER: PF-0066 US
37      (ix) TELECOMMUNICATION INFORMATION:
38           (A) TELEPHONE: 415-855-0555
39           (B) TELEFAX: 415-845-4166
41 (2) INFORMATION FOR SEQ ID NO: 1:
43       (i) SEQUENCE CHARACTERISTICS:
44           (A) LENGTH: 131 amino acids
45           (B) TYPE: amino acid
46           (C) STRANDEDNESS: single
47           (D) TOPOLOGY: linear
49      (ii) MOLECULE TYPE: peptide
51     (vii) IMMEDIATE SOURCE:
52           (A) LIBRARY: SCAH-1
53           (B) CLONE:
55      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57 Met Lys Ile Phe Leu Pro Val Leu Leu Ala Ala Leu Leu Gly Val Glu
58  1               5                  10                  15
59 Arg Ala Ser Ser Leu Met Cys Phe Ser Cys Leu Asn Gln Lys Ser Asn
60             20                  25                  30
61 Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys
62             35                  40                  45
```

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PATENT APPLICATION: US/09/934,586   TIME: 13:54:13

Input Set : N:\Crf3\RULE60\09934586.txt
Output Set: N:\CRF3\10162001\I934586.raw

```
 63  Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly
 64      50                  55                  60
 65  His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly
 66  65                  70                  75                  80
 67  Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe
 68                  85                  90                  95
 69  Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr
 70                  100                 105                 110
W--> 71 Leu Leu Gly Ala Gly Leu Leu Leu Ser Leu Xaa Pro Ala Leu Leu Arg
 72          115                 120                 125
 73  Phe Gly Pro
 74      130
 76 (2) INFORMATION FOR SEQ ID NO: 2:
 78      (i) SEQUENCE CHARACTERISTICS:
 79          (A) LENGTH: 123 amino acids
 80          (B) TYPE: amino acid
 81          (C) STRANDEDNESS: single
 82          (D) TOPOLOGY: linear
 84     (ii) MOLECULE TYPE: peptide
 86    (vii) IMMEDIATE SOURCE:
 87          (A) LIBRARY: SCAH-2
 88          (B) CLONE:
 90     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 92  Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
 93  1               5                   10                  15
 94  Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
 95              20                  25                  30
 96  Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
·97              35                  40                  45
 98  Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
 99      50                  55                  60
 100 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
 101 65                  70                  75                  80
W--> 102 Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Xaa Ser Gly
 103                 85                  90                  95
 104 Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
 105                 100                 105                 110
 106 Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
 107             115                 120
 109 (2) INFORMATION FOR SEQ ID NO: 3:
 111     (i) SEQUENCE CHARACTERISTICS:
 112         (A) LENGTH: 537 base pairs
 113         (B) TYPE: nucleic acid
 114         (C) STRANDEDNESS: single
 115         (D) TOPOLOGY: linear
 117    (ii) MOLECULE TYPE: cDNA
 119   (vii) IMMEDIATE SOURCE:
 120         (A) LIBRARY: SCAH-1
 121         (B) CLONE:
```

RAW SEQUENCE LISTING   DATE: 10/16/2001
PATENT APPLICATION: US/09/934,586   TIME: 13:54:13

Input Set : N:\Crf3\RULE60\09934586.txt
Output Set: N:\CRF3\10162001\I934586.raw

```
123     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
125  NAGGANGGTG GGGGACCCAN GGGTCCAGAG CGCAGTTCGG GTCGGAGCTY CGWCCAGGCT    60
126  GCTGGTACCT GCGTCCGCCC GGCGAGCAGG ACAGGCTGCT TTGGTTTGTG ACCTCCAGGC   120
127  AGGACGGCCA TCCTCTCCAG AATGAAGATC TTCTTGCCAG TGCTGCTGGC TGCCCTTCTG   180
128  GGTGTGGAGC GAGCCAGCTC GCTGATGTGC TTCTCCTGCT TGAACCAGAA GAGCAATCTG   240
129  TACTGCCTGA AGCCGACCAT CTGCTCCGAC CAGGACAACT ACTGCGTGAC TGTGTCTGCT   300
130  AGTGCCGGCA TTGGGAATCT CGTGACATTT GGCCACAGCC TGAGCAAGAC CTGTTCCCCG   360
131  GCCTGCCCCA TCCCAGAAGG CGTCAATGTT GGTGTGGCTT CCATGGGCAT CAGCTGCTGC   420
132  CAGAGCTTTC TGTGCAATTT CAGTGCGGCC GATGGCGGGC TGCGGGCAAG CGTCACCCTG   480
133  CTGGGTGCCG GGCTGCTGCT GAGCCTGWTG CCGGCCCTGC TGCGGTTTGG CCCCTGA      537
135  (2) INFORMATION FOR SEQ ID NO: 4:
137      (i) SEQUENCE CHARACTERISTICS:
138          (A) LENGTH: 494 base pairs
139          (B) TYPE: nucleic acid
140          (C) STRANDEDNESS: single
141          (D) TOPOLOGY: linear
143     (ii) MOLECULE TYPE: cDNA
145    (vii) IMMEDIATE SOURCE:
146          (A) LIBRARY: SCAH-2
147          (B) CLONE:
149     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
151  GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC    60
152  ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG   120
153  GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC   180
154  CTGACCGTCA TCAGCAAAGG CTGCAGCTTG AACTGCGTGG ATGACTCACA GGACTACTAC   240
155  GTGGGCAAGA AGAACATCAC GTGCTGTGAC ACCGACTTGT GCAACGSCAG CGGGGCCCAT   300
156  GCCCTGCAGC CGGCTGCCGC CATCCTTGCG CTGCTCCCTG CACTCGGCCT GCTGCTCTGG   360
157  GGACCCGGCC AGCTATAGGC TCTGGGGGGC CCCGMTGCAG CCCACACTGG GTGTGGTGCC   420
158  CCAAGGCCTC TGTGSCACTC CTMACAGACC TGGGCCCAGT GGGAGSCTGT CTCTNGGTTC   480
159  CTGAGGCACA TCCT                                                      494
161  (2) INFORMATION FOR SEQ ID NO: 5:
163      (i) SEQUENCE CHARACTERISTICS:
164          (A) LENGTH: 136 amino acids
165          (B) TYPE: amino acid
166          (C) STRANDEDNESS: single
167          (D) TOPOLOGY: linear
169     (ii) MOLECULE TYPE: peptide
171    (vii) IMMEDIATE SOURCE:
172          (A) LIBRARY: GenBank
173          (B) CLONE: 434660
175     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
177  Met Ser Ala Thr Ser Asn Met Arg Val Phe Leu Pro Val Leu Leu Ala
178   1               5                  10                  15
179  Ala Leu Leu Gly Met Glu Gln Val His Ser Leu Met Cys Phe Ser Cys
180              20                  25                  30
181  Thr Asp Gln Lys Asn Asn Ile Asn Cys Leu Trp Pro Val Ser Cys Gln
182              35                  40                  45
183  Glu Lys Asp His Tyr Cys Ile Thr Leu Ser Ala Ala Ala Gly Phe Gly
184       50                  55                  60
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/934,586

DATE: 10/16/2001
TIME: 13:54:13

Input Set : N:\Crf3\RULE60\09934586.txt
Output Set: N:\CRF3\10162001\I934586.raw

```
185 Asn Val Asn Leu Gly Tyr Thr Leu Asn Lys Gly Cys Ser Pro Ile Cys
186 65              70              75              80
187 Pro Ser Glu Asn Val Asn Leu Asn Leu Gly Val Ala Ser Val Asn Ser
188              85              90              95
189 Tyr Cys Cys Gln Ser Ser Phe Cys Asn Phe Ser Ala Ala Gly Leu Gly
190              100             105             110
191 Leu Arg Ala Ser Ile Pro Leu Leu Gly Leu Gly Leu Leu Leu Ser Leu
192          115             120             125
193 Leu Ala Leu Leu Gln Leu Ser Pro
194      130             135 .
196 (2) INFORMATION FOR SEQ ID NO: 6:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 109 amino acids
200          (B) TYPE: amino acid
201          (C) STRANDEDNESS: single
202          (D) TOPOLOGY: linear
204     (ii) MOLECULE TYPE: peptide
206    (vii) IMMEDIATE SOURCE:
207          (A) LIBRARY: GenBank
208          (B) CLONE: 1199651
210     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
212 Met Ser Thr Thr Ser Ser Met Arg Val Phe Ser Ile Val Leu Gln Ala
213 1               5               10              15
214 His Leu Leu Gly Val Glu Leu Val Pro Ser Leu Ile Cys Ser Ser Cys
215              20              25              30
216 Thr His Gln Lys Ser Asn Ile Asn Pro Pro Trp Pro Val Ala Cys Lys
217          35              40              45
218 Asp Thr Gly Asn Tyr Cys Ile Met Leu Phe Ser Ala Val Gly Phe Gly
219      50              55              60
220 Asn Val Asn Leu Gly Tyr Thr Leu Asn Thr Gly Cys Ser Gln Ser Cys
221 65              70              75              80
222 Pro His Glu Asn Ile Asn Ile Asn Pro Gly Val Ala Ser Val Asn Ser
223              85              90              95
224 Tyr Gln Ser Ser Phe Cys Asn Phe Ser Asn Ala Cys Leu
225              100             105
227 (2) INFORMATION FOR SEQ ID NO: 7:
229      (i) SEQUENCE CHARACTERISTICS:
230          (A) LENGTH: 148 base pairs
231          (B) TYPE: nucleic acid
232          (C) STRANDEDNESS: single
233          (D) TOPOLOGY: linear
235     (ii) MOLECULE TYPE: cDNA
237    (vii) IMMEDIATE SOURCE:
238          (A) LIBRARY: THP1PEB01
239          (B) CLONE: 72518
241     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
243 CCTGAAGCCG ACCATCTGNT CCGACCAGGN CAACTACTGN GTGACTGTGT CTGCTAGTGC    60
244 CGGCATTTGG AATCTTGTGC CATTTNGACA CAGCCTNAGC AAGACCTNTT CCCCGGCCTN   120
245 NCCCATCCCA GAAGGNGTCA ATNATNGT                                      148
```

RAW SEQUENCE LISTING   DATE: 10/16/2001
PATENT APPLICATION: US/09/934,586   TIME: 13:54:13

Input Set : N:\Crf3\RULE60\09934586.txt
Output Set: N:\CRF3\10162001\I934586.raw

```
247 (2) INFORMATION FOR SEQ ID NO: 8:
249      (i) SEQUENCE CHARACTERISTICS:
250          (A) LENGTH: 196 base pairs
251          (B) TYPE: nucleic acid
252          (C) STRANDEDNESS: single
253          (D) TOPOLOGY: linear
255      (ii) MOLECULE TYPE: cDNA
257      (vii) IMMEDIATE SOURCE:
258          (A) LIBRARY: THP1PLB02
259          (B) CLONE: 155838
261      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
263 CGGACAGGCT GCTTTGGTTT GTNACCTCCA GGCAGGACGG CCATCCTCTC CAGAATGAAG      60
264 ATCTTCTTGC CANTGCTGCT GGCTGCCCTT CTNGGTGTGG AGCGAGCCAG CTCGCTGATG     120
265 TGCTTCTCCT GCTTNAACCA GAAGAGCAAT CTGTACTGCC TGAAGCCGAC CATCTGCTCC     180
266 GACCAGGNCA ACTACT                                                     196
268 (2) INFORMATION FOR SEQ ID NO: 9:
270      (i) SEQUENCE CHARACTERISTICS:
271          (A) LENGTH: 278 base pairs
272          (B) TYPE: nucleic acid
273          (C) STRANDEDNESS: single
274          (D) TOPOLOGY: linear
276      (ii) MOLECULE TYPE: cDNA
278      (vii) IMMEDIATE SOURCE:
279          (A) LIBRARY: HNT2RAT01
280          (B) CLONE: 486681
282      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
284 GTTCGGGGAG CTCGGCCAGG CTGCTGGTAC CTGCGTCCGC CCGGCGAGCA GGACAGGCTG      60
285 CTTTGGTTTG TGACCTNCAG GCAGGACGGC CATCCTCTNC AGAATGAAGA TCTTCTTGCC     120
286 AGTGCTGCTG GNTGCCCTTC TGGGTGTGGA GCGAGCCAGC TNGCTGATGT GCTTCTTCTG     180
287 CTTGAACCAG AAGAGCAATC TGTACTGCTG AAGCCGACCA TCTGTTCGAC CAGGNCAACT     240
288 ACTGCGTGAC TGTGTCTGCT AGTGNCGGCA TTGGGAAT                             278
290 (2) INFORMATION FOR SEQ ID NO: 10:
292      (i) SEQUENCE CHARACTERISTICS:
293          (A) LENGTH: 262 base pairs
294          (B) TYPE: nucleic acid
295          (C) STRANDEDNESS: single
296          (D) TOPOLOGY: linear
298      (ii) MOLECULE TYPE: cDNA
300      (vii) IMMEDIATE SOURCE:
301          (A) LIBRARY: BRSTTUT01
302          (B) CLONE: 604702
304      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
306 GGTTCGGGGA GCTCGGCCAG GCTGCTGGTA CCTGCGTCCG CCCGGCGAGC AGGACAGGCT      60
307 GCTTTGGTTT GTGACCTCCA GGCAGGACGG CCATCCTCTC CAGAATGAAG ATCTTCTTGC     120
308 CAGTGCTGCT GGCTGCCCTT CTGGGTGTGG AGCGAGCCAG CTCGCTGATG TGCTTCTCCT     180
309 GCTTGAACCA GAAGAGCAAT CTGTACTGCC TGAAGCCGAC CATCTGCTCC GACCAGGACA     240
310 ACTACTGCGT GACTGTGTCT GC                                              262
312 (2) INFORMATION FOR SEQ ID NO: 11:
314      (i) SEQUENCE CHARACTERISTICS:
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VERIFICATION SUMMARY   DATE: 10/16/2001
PATENT APPLICATION: **US/09/934,586**   TIME: 13:54:14

Input Set : **N:\Crf3\RULE60\09934586.txt**
Output Set: **N:\CRF3\10162001\I934586.raw**

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2